

Figure S3. Rescaled Slatkin-Maddison's s (σ) plotted against the spatial distance between two localities. Estimates from different gene segment data sets are shown in different rows. The left column shows the plot of σ between each pair of localities against their spatial distance (km). The middle column shows the median σ estimates (black circles with lines) and their frequencies (bars) in bins of spatial distance (500 km) between the localities compared. The right column shows σ plotted against the spatial distance (km) between all pairs of the four localities (Alaska-AK, Washington-WA, California-CA and Oregon-OR) in the Pacific Flyway only. Error bars on the left and right columns show the upper and lower 95% of the σ estimates from 200 randomly selected bootstrap replicates. The error bars in the middle column show the standard error of the σ estimate assuming a normal distribution. Red straight lines are the linear regressions of σ values, with Pearson's correlations (R) also shown. The significance of the correlation between the level of gene flow and spatial distance in the matrix was assessed using a Mantel test (p values < 0.05). In the PA (Lineage A) data set, the estimate of gene flow between Oregon and North Dakota was omitted due to its extremely large uncertainty (95% CI > 2.0). Some less frequently sampled states ($3 \leq n \leq 5$) were included in N6 and N8.

